

115 000



PCT

RAW SEQUENCE LISTING

DATE: 02/11/2003

PATENT APPLICATION: US/09/720,560

TIME: 08:57:56

Input Set : A:\ACY33427USPCT.Seq.txt

Output Set: N:\CRF4\02102003\I720560.raw

4 <110> APPLICANT: American Cyanamid Company
 5 Fulginiti, James P.
 6 Fiske, Michael J.
 7 Diltz, Deborah A.
 9 <120> TITLE OF INVENTION: NOVEL ANTIGENS OF HELICOBACTER PYLORI
 12 <130> FILE REFERENCE: 0646/8D941
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/720,560
 C--> 15 <141> CURRENT FILING DATE: 2002-12-11
 17 <150> PRIOR APPLICATION NUMBER: 60/090,851
 18 <151> PRIOR FILING DATE: 1998-06-26
 20 <160> NUMBER OF SEQ ID NOS: 42
 22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 708
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Helicobacter pylori
 29 <400> SEQUENCE: 1

30	Met	Lys	Lys	Thr	Leu	Leu	Leu	Ser	Leu	Ser	Leu	Ser	Phe	Leu
31	1				5				10				15	
32	Leu	His	Ala	Glu	Asp	Asp	Gly	Phe	Tyr	Thr	Ser	Val	Gly	Tyr
33				20					25				30	Gln
34	Gly	Glu	Ala	Ala	Gln	Met	Val	Lys	Asn	Thr	Lys	Gly	Ile	Gln
35				35					40				45	Glu
36	Ser	Asp	Asn	Tyr	Glu	Lys	Leu	Asn	Asn	Leu	Leu	Asn	Asn	Tyr
37				50					55				60	Ser
38	Leu	Asn	Thr	Leu	Ile	Lys	Leu	Ser	Ala	Asp	Pro	Ser	Ala	Ile
39	65				70				75				80	Asn
40	Ala	Arg	Asp	Asn	Leu	Gly	Ser	Ser	Arg	Asn	Leu	Leu	Asp	Val
41				85					90				95	Lys
42	Thr	Asn	Ser	Pro	Ala	Tyr	Gln	Ala	Val	Leu	Leu	Ala	Leu	Asn
43				100					105				110	Ala
44	Val	Gly	Leu	Trp	Gln	Val	Thr	Ser	Tyr	Ala	Phe	Thr	Ala	Cys
45				115					120				125	Gly
46	Gly	Ser	Asn	Glu	Asn	Ala	Asn	Gly	Gly	Ile	Gln	Thr	Phe	Asn
47				130					135				140	Asn
48	Pro	Gly	Gln	Asp	Thr	Thr	Ile	Thr	Cys	Asn	Ser	Tyr	Tyr	Glu
49	145				150				155				160	Pro
50	Gly	His	Gly	Gly	Pro	Ile	Ser	Thr	Ala	Asn	Tyr	Ala	Lys	Ile
51				165					170				175	Asn
52	Ala	Tyr	Gln	Ile	Ile	Gln	Lys	Ala	Leu	Thr	Ala	Asn	Gly	Ala
53				180					185				190	Gly
54	Asp	Gly	Val	Pro	Val	Leu	Ser	Asn	Thr	Thr	Thr	Lys	Leu	Asp
55				195					200				205	Thr

P.6

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56 Ile Asn Gly Asp Lys Arg Thr Gly Gly Lys Pro Asn Thr Pro Glu Lys
57      210                      215                      220
58 Phe Pro Trp Ser Asp Gly Lys Tyr Ile His Thr Gln Trp Ile Asn Thr
59 225                      230                      235                      240
60 Ile Val Thr Pro Thr Glu Thr Asn Ile Asn Thr Glu Asn Asn Ala Gln
61                      245                      250                      255
62 Glu Leu Leu Lys Gln Ala Ser Ile Ile Ile Thr Thr Leu Asn Glu Ala
63                      260                      265                      270
64 Cys Pro Asn Phe Gln Asn Gly Gly Arg Ser Tyr Trp Gln Gly Ile Ser
65                      275                      280                      285
66 Gly Asn Gly Thr Met Cys Gly Met Phe Lys Asn Glu Ile Ser Ala Ile
67      290                      295                      300
68 Gln Gly Met Ile Ala Asn Ala Gln Glu Ala Val Ala Gln Ser Lys Ile
69 305                      310                      315                      320
70 Val Ser Glu Asn Ala Gln Asn Gln Asn Asn Leu Asp Thr Gly Lys Pro
71                      325                      330                      335
72 Phe Asn Pro Tyr Thr Asp Ala Ser Phe Ala Gln Ser Met Leu Lys Asn
73                      340                      345                      350
74 Ala Gln Ala Gln Ala Glu Ile Leu Asn Gln Ala Glu Gln Val Val Lys
75                      355                      360                      365
76 Asn Phe Glu Lys Ile Pro Thr Ala Phe Val Ser Asp Ser Leu Gly Val
77      370                      375                      380
78 Cys Tyr Glu Val Gln Gly Gly Glu Arg Arg Gly Thr Asn Pro Gly Gln
79 385                      390                      395                      400
80 Val Thr Ser Asn Thr Trp Gly Ala Gly Cys Ala Tyr Val Lys Gln Thr
81                      405                      410                      415
82 Ile Thr Asn Leu Asp Asn Ser Ile Ala His Phe Gly Thr Gln Glu Gln
83                      420                      425                      430
84 Gln Ile Gln Gln Ala Glu Asn Ile Ala Asp Thr Leu Val Asn Phe Lys
85                      435                      440                      445
86 Ser Arg Tyr Ser Glu Leu Gly Asn Thr Tyr Asn Ser Ile Thr Thr Ala
87      450                      455                      460
88 Leu Ser Lys Val Pro Asn Ala Gln Ser Leu Gln Asn Val Val Ser Lys
89 465                      470                      475                      480
90 Lys Asn Asn Pro Tyr Ser Pro Gln Gly Ile Glu Thr Asn Tyr Tyr Leu
91                      485                      490                      495
92 Asn Gln Asn Ser Tyr Asn Gln Ile Gln Thr Ile Asn Gln Glu Leu Gly
93                      500                      505                      510
94 Arg Asn Pro Phe Arg Lys Val Gly Ile Val Asn Ser Gln Thr Asn Asn
95      515                      520                      525
96 Gly Ala Met Asn Gly Ile Gly Ile Gln Val Gly Tyr Lys Gln Phe Phe
97      530                      535                      540
98 Gly Gln Lys Arg Lys Trp Gly Ala Arg Tyr Tyr Gly Phe Phe Asp Tyr
99 545                      550                      555                      560
100 Asn His Ala Phe Ile Lys Ser Ser Phe Phe Asn Ser Ala Ser Asp Val
101                      565                      570                      575
102 Trp Thr Tyr Gly Phe Gly Ala Asp Ala Leu Tyr Asn Phe Ile Asn Asp
103                      580                      585                      590
104 Lys Ala Thr Asn Phe Leu Gly Lys Asn Asn Lys Leu Ser Val Gly Leu

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105          595          600          605
106 Phe Gly Gly Ile Ala Leu Ala Gly Thr Ser Trp Leu Asn Ser Glu Tyr
107          610          615          620
108 Val Asn Leu Ala Thr Val Asn Asn Val Tyr Asn Ala Lys Met Asn Val
109 625          630          635          640
110 Ala Asn Phe Gln Phe Leu Phe Asn Met Gly Val Arg Met Asn Leu Ala
111          645          650          655
112 Arg Ser Lys Lys Lys Gly Ser Asp His Ala Ala Gln His Gly Ile Glu
113          660          665          670
114 Leu Gly Leu Lys Ile Pro Thr Ile Asn Thr Asn Tyr Tyr Ser Phe Met
115          675          680          685
116 Gly Ala Glu Leu Lys Tyr Arg Arg Leu Tyr Ser Val Tyr Leu Asn Tyr
117          690          695          700
118 Val Phe Ala Tyr
119 705
121 <210> SEQ ID NO: 2
122 <211> LENGTH: 741
123 <212> TYPE: PRT
124 <213> ORGANISM: Helicobacter pylori
126 <400> SEQUENCE: 2
127 Met Lys Lys His Ile Leu Ser Leu Ala Leu Gly Ser Leu Leu Val Ser
128 1          5          10          15
129 Thr Leu Ser Ala Glu Asp Asp Gly Phe Tyr Thr Ser Val Gly Tyr Gln
130          20          25          30
131 Ile Gly Glu Ala Ala Gln Met Val Thr Asn Thr Lys Gly Ile Gln Asp
132          35          40          45
133 Leu Ser Asp Arg Tyr Glu Ser Leu Asn Asn Leu Leu Thr Arg Tyr Ser
134          50          55          60
135 Thr Leu Asn Thr Leu Ile Lys Leu Ser Ala Asp Pro Ser Ala Ile Asn
136 65          70          75          80
137 Ala Ala Arg Glu Asn Leu Gly Ala Ser Ala Lys Asn Leu Ile Gly Asp
138          85          90          95
139 Lys Ala Asn Ser Pro Ala Tyr Gln Ala Val Leu Leu Ala Ile Asn Ala
140          100          105          110
141 Ala Val Gly Phe Trp Asn Val Leu Gly Tyr Ala Thr Gln Cys Gly Gly
142          115          120          125
143 Asn Ala Asn Gly Gln Lys Ser Thr Ser Ser Thr Thr Ile Phe Asn Asn
144          130          135          140
145 Glu Pro Gly Tyr Arg Ser Thr Ser Ile Thr Cys Ser Leu Asn Gly Tyr
146 145          150          155          160
147 Thr Pro Gly Tyr Tyr Gly Pro Met Ser Ile Glu Asn Phe Lys Lys Leu
148          165          170          175
149 Asn Glu Ala Tyr Gln Ile Leu Gln Thr Ala Leu Lys Gln Gly Leu Pro
150          180          185          190
151 Ala Leu Lys Glu Asn Asn Lys Lys Val Asn Val Thr Tyr Thr Tyr Thr
152          195          200          205
153 Cys Ser Gly Gly Gly Asn Asn Asn Cys Ser Ser Glu Ala Thr Gly Val
154          210          215          220
155 Ser Asn Gln Asn Gly Gly Thr Lys Thr Thr Thr Gln Thr Ile Asp Gly

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156	225				230				235			240				
157	Lys	Ser	Val	Thr	Thr	Thr	Ile	Ser	Ser	Lys	Val	Val	Asp	Ser	Thr	Ala
158					245				250						255	
159	Ser	Gly	Asn	Thr	Ser	Arg	Val	Ser	Tyr	Thr	Glu	Ile	Thr	Asn	Lys	Leu
160				260					265					270		
161	Glu	Gly	Val	Pro	Asp	Ser	Ala	Gln	Ala	Leu	Leu	Ala	Gln	Ala	Ser	Thr
162			275					280					285			
163	Leu	Ile	Ser	Thr	Ile	Asn	Thr	Ala	Cys	Pro	Phe	Phe	Ser	Val	Thr	Asn
164		290					295					300				
165	Gln	Ser	Gly	Gly	Pro	Gln	Met	Glu	Pro	Thr	Lys	Gly	Lys	Leu	Cys	Gly
166	305					310					315				320	
167	Phe	Thr	Glu	Glu	Ile	Ser	Ala	Ile	Gln	Lys	Met	Ile	Thr	Asp	Ala	Gln
168				325					330					335		
169	Glu	Leu	Val	Asn	Gln	Thr	Ser	Val	Ile	Asn	Ser	His	Glu	Gln	Ser	Thr
170			340						345				350			
171	Leu	Val	Gly	Gly	Asn	Asn	Gly	Lys	Pro	Phe	Asn	Pro	Phe	Thr	Asp	Ala
172		355					360					365				
173	Gln	Phe	Ala	Gln	Gly	Met	Leu	Ala	Asn	Ala	Ser	Ala	Gln	Ala	Lys	Met
174		370					375					380				
175	Leu	Asn	Leu	Ala	His	Gln	Val	Gly	Gln	Thr	Ile	Asn	Pro	Asn	Asn	Leu
176	385					390				395				400		
177	Thr	Gly	Asn	Phe	Lys	Asn	Phe	Val	Thr	Gly	Phe	Leu	Ala	Thr	Cys	Asn
178			405						410				415			
179	Asn	Pro	Ser	Thr	Ala	Gly	Thr	Gly	Gly	Thr	Gln	Gly	Ser	Ala	Pro	Gly
180			420						425				430			
181	Thr	Val	Thr	Thr	Gln	Thr	Phe	Ala	Ser	Gly	Cys	Ala	Tyr	Val	Glu	Gln
182		435					440					445				
183	Thr	Ile	Thr	Asn	Leu	Glu	Asn	Ser	Ile	Ala	His	Phe	Gly	Thr	Gln	Glu
184		450				455					460					
185	Gln	Gln	Ile	Gln	Arg	Ala	Glu	Asn	Ile	Ala	Asp	Thr	Leu	Val	Asn	Phe
186	465				470					475					480	
187	Lys	Ser	Arg	Tyr	Ser	Glu	Leu	Gly	Asn	Thr	Tyr	Asn	Ser	Ile	Thr	Thr
188			485						490				495			
189	Ala	Leu	Ser	Lys	Val	Pro	Asn	Ala	Gln	Ser	Leu	Gln	Asn	Val	Val	Ser
190			500						505				510			
191	Lys	Lys	Asn	Asn	Pro	Tyr	Ser	Pro	Gln	Gly	Ile	Glu	Thr	Asn	Tyr	Tyr
192			515					520				525				
193	Leu	Asn	Gln	Asn	Ser	Tyr	Asn	Gln	Ile	Gln	Thr	Ile	Asn	Gln	Glu	Leu
194		530					535					540				
195	Gly	Arg	Asn	Pro	Phe	Arg	Lys	Val	Gly	Ile	Val	Gly	Ser	Gln	Thr	Asn
196	545				550					555				560		
197	Asn	Gly	Ala	Met	Asn	Gly	Ile	Gly	Ile	Gln	Val	Gly	Tyr	Glu	Gln	Phe
198			565						570				575			
199	Phe	Gly	Gln	Lys	Arg	Lys	Trp	Gly	Ala	Arg	Tyr	Tyr	Gly	Phe	Phe	Asp
200			580					585					590			
201	Tyr	Asn	His	Ala	Phe	Ile	Lys	Ser	Phe	Phe	Asn	Ser	Ala	Ser	Asp	
202		595					600					605				
203	Val	Trp	Thr	Tyr	Gly	Phe	Gly	Ala	Asp	Ala	Leu	Tyr	Asn	Phe	Ile	Asn
204		610					615					620				

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205 Asp Lys Ala Thr Asn Phe Leu Gly Lys Asn Asn Lys Leu Ser Val Gly
206 625 630 635 640
207 Leu Phe Gly Gly Ile Ala Leu Ala Gly Thr Ser Trp Leu Asn Ser Glu
208 645 650 655
209 Tyr Val Asn Leu Ala Thr Val Asn Asn Val Tyr Asn Ala Lys Met Asn
210 660 665 670
211 Val Ala Asn Phe Gln Phe Leu Phe Asn Met Gly Val Arg Met Asn Leu
212 675 680 685
213 Ala Arg Pro Lys Lys Asn Asp Ser Asp His Ala Ala Gln His Gly Ile
214 690 695 700
215 Glu Leu Gly Leu Lys Ile Pro Thr Ile Asn Thr Asn Tyr Tyr Ser Phe
216 705 710 715 720
217 Met Gly Ala Glu Leu Lys Tyr Arg Arg Leu Tyr Ser Val Tyr Leu Asn
218 725 730 735
219 Tyr Val Phe Ala Tyr
220 740
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 745
224 <212> TYPE: PRT
225 <213> ORGANISM: Helicobacter pylori
227 <400> SEQUENCE: 3
228 Met Lys Lys His Ile Leu Ser Leu Ala Leu Gly Ser Leu Leu Val Ser
229 1 5 10 15
230 Thr Leu Ser Ala Glu Asp Asp Gly Phe Tyr Thr Ser Val Gly Tyr Gln
231 20 25 30
232 Ile Gly Glu Ala Ala Gln Met Val Thr Asn Thr Lys Gly Ile Gln Gln
233 35 40 45
234 Leu Ser Asp Asn Tyr Glu Asn Leu Asn Asn Leu Leu Thr Arg Tyr Ser
235 50 55 60
236 Thr Leu Asn Thr Leu Ile Lys Leu Ser Ala Asp Pro Ser Ala Ile Asn
237 65 70 75 80
238 Ala Val Arg Glu Asn Leu Gly Ala Ser Thr Lys Asn Leu Ile Gly Asp
239 85 90 95
240 Lys Ala Asn Ser Pro Ala Tyr Gln Ala Val Phe Leu Ala Ile Asn Ala
241 100 105 110
242 Ala Val Gly Leu Trp Asn Thr Ile Gly Tyr Ala Val Met Cys Gly Asn
243 115 120 125
244 Gly Asn Gly Thr Glu Ser Gly Pro Gly Ser Val Ile Phe Asn Asp Gln
245 130 135 140
246 Pro Gly Gln Asp Ser Thr Gln Ile Thr Cys Asn Arg Phe Glu Ser Thr
247 145 150 155 160
248 Gly Pro Gly Lys Ser Met Ser Ile Asp Glu Phe Lys Lys Leu Asn Glu
249 165 170 175
250 Ala Tyr Gln Ile Ile Gln Gln Ala Leu Lys Asn Gln Ser Gly Phe Pro
251 180 185 190
252 Glu Leu Gly Gly Asn Gly Thr Lys Val Ser Val Asn Tyr Asn Tyr Glu
253 195 200 205
254 Cys Arg Gln Thr Ala Asp Ile Asn Gly Gly Val Tyr Gln Phe Cys Lys
255 210 215 220

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/720,560

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:33; N Pos. 12,21,24,27,30,42,48,51,60